Listing of the Claims

This listing of claims will replace all prior versions, and listings of claims in the application.

1 - 48. (Cancelled)

49. (Previously presented) A method for recovering one or more circular target nucleic acid molecules, said method comprising:

(A) obtaining a sample comprising one or more single-stranded circular target nucleic acid molecules;

(B) incubating said sample in the presence of one or more haptenylated nucleic acid probe molecules under conditions sufficient to permit one or more of said probe molecules to hybridize to one or more of said circular target nucleic acid molecules, thereby forming one or more hybridized probe-target molecules;

(C) capturing one or more of said hybridized probe-target molecules in the presence of one or more binding ligands which are capable of binding to the hapten of said one or more haptenylated nucleic acid probe molecules, wherein one or more of said binding ligands are conjugated to a support, thereby forming one or more captured hybridized probe-target molecules;

(D) incubating one or more of said captured hybridized probe-target molecules under conditions sufficient to permit release of one or more of said haptenylated nucleic acid probe molecules from one or more of said circular target nucleic acid molecules; and

(E) treating said circular target nucleic acid molecules obtained in (D) under conditions sufficient to make one or more of said circular target nucleic acid molecules double-stranded.

50. (Previously presented) The method of claim 49, further comprising transforming a host cell with one or more of said double-stranded circular target nucleic acid molecules obtained in (E).

51. (Previously presented) The method of claim 49, wherein said incubation in (B) is under conditions which minimize random hybridization.

52. (Previously presented) The method of claim 49, wherein one or more of said circular target nucleic acid molecules are DNA molecules.

53. (Previously presented) The method of claim 49, wherein said sample comprises a mixture or library of DNA molecules.

54. (Previously presented) The method of claim 49, wherein one or more of said circular target nucleic acid molecules are selected from the group consisting of plasmids, cosmids and phagemids.

55. (Previously presented) The method of claim 49, wherein one or more of said circular target nucleic acid molecules are plasmids.

56. (Previously presented) The method of claim 49, wherein one or more of said circular target nucleic acid molecules are cosmids.

57. (Previously presented) The method of claim 49, wherein one or more of said circular target nucleic acid molecules are phagemids.

58. (Cancelled)

59. (Previously presented) The method of claim 49, wherein said hapten is biotin.

60. (Previously presented) The method of claim 59, wherein said biotin is covalently bonded to the 3' terminus of said one or more haptenylated nucleic acid probe molecules.

61. (Previously presented) The method of claim 49, wherein said one or more

binding ligands are selected from the group consisting of avidin, streptavidin, antibodies that bind biotin and antibody fragments that bind biotin.

62. (Previously presented) The method of claim 49, wherein said one or more binding ligands are avidin.

63. (Previously presented) The method of claim 49, wherein said one or more binding ligands are streptavidin.

64. (Previously presented) The method of claim 49, wherein said one or more binding ligands are antibodies that bind biotin.

65. (Previously presented) The method of claim 49, wherein said one or more binding ligands are antibody fragments that bind biotin.

66. (Previously presented) The method of claim 49, wherein said support is a paramagnetic bead.

67. (Previously presented) The method of claim 49, wherein one or more of said haptenylated nucleic acid probe molecules has a degenerate sequence.

68. (Previously presented) The method of claim 49, wherein said sample comprising one or more single-stranded circular target nucleic acid molecules is obtained in (A) by subjecting a sample comprising one or more double-stranded circular nucleic acid molecules to conditions which denature said double-stranded molecules into their respective single strands.